Run on: March 26, 2005, 14:36:30 ; Search time 22 Seconds
                                           (without alignments)
                                           78.042 Million cell
updates/sec

Title: US-10-009-643-5
Perfect score: 111
Sequence: 1 SKAYRKLLGQLSARLYLHSLMAK 23

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 500 summaries

Database :   Issued_Patents_AA:*
                 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
                 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
                 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
                 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
                 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being
printed,
     and is derived by analysis of the total score distribution.

                              SUMMARIES

            %
Result   Query
  No. Score Match Length DB ID   Description

----
      1   104 93.7   29 3 US-08-789-329C-20   Sequence 20,
Appl
      2   104 93.7   43 3 US-08-789-329C-8   Sequence 8,
Appli
      3   104 93.7   46 3 US-08-789-329C-4   Sequence 4,
Appli
      4   104 93.7   172 3 US-08-789-329C-7   Sequence 7,
Appli
      5   104 93.7   175 3 US-08-789-329C-3   Sequence 3,
Appli
      6   97 87.4   45 1 US-08-062-472B-8   Sequence 8,
Appli
      7   97 87.4   173 1 US-08-062-472B-6   Sequence 6,
Appli
      8   96 86.5   45 1 US-08-062-472B-25   Sequence 25,
Appl
      9   96 86.5   113 1 US-08-062-472B-11   Sequence 11,

Run on: March 26, 2005, 14:37:35 ; Search time 48 Seconds
                                            (without alignments)
                                            158.653 Million cell
updates/sec

Title: US-10-009-643-5
Perfect score: 111
Sequence: 1 SKAYRKLLGQLSARLYLHSLMAK 23

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 1407402 seqs, 331100923 residues

Total number of hits satisfying chosen parameters: 1407402

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 500 summaries

Database :   Published_Applications_AA:*
                 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
                 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
                 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
                 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
                 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
                 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
                 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
                 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
                 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
                 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
                 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
                 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
                 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
                 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
                 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
                 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
                 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
                 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
                 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
                 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

    Pred. No. is the number of results predicted by chance to have a
    score greater than or equal to the score of the result being
printed,
    and is derived by analysis of the total score distribution.

                              SUMMARIES
                    %
Result   Query
   No.   Score   Match   Length   DB   ID   Description

----
     1   67   60.4   170   17   US-10-686-282-15   Sequence
15, Appl
     2   67   60.4   170   17   US-10-686-282-17   Sequence

Run on: March 26, 2005, 14:36:00 ; Search time 16 Seconds
                                          (without alignments)
                                          138.312 Million cell
updates/sec

Title: US-10-009-643-5
Perfect score: 111
Sequence: 1 SKAYRKLLGQLSARLYLHSLMAK 23

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 500 summaries

Database :   PIR_79:*
                 1: pir1:*
                 2: pir2:*
                 3: pir3:*
                 4: pir4:*
                                          SUMMARIES
                 %
Result   Query
  No.   Score   Match Length DB   ID   Description

----
      1   97   87.4   173 2   S34767   neuropeptides
prec
      2   80   72.1   176 2   A34044   pituitary
adenylat
      3   71   64.0   175 2   A37786   pituitary
adenylat
      4   67   60.4   145 2   A60038   vasoactive
intesti
      5   67   60.4   170 1   VRHU   vasoactive
intesti
      6   63   56.8   44 1   RHPG   somatoliberin
- pi
      7   63   56.8   108 1   RHHUS   somatoliberin
prec
      8   62   55.9   55 1   VRGP   vasoactive
intesti
      9   62   55.9   170 1   VRRT   vasoactive
intesti
     10   62   55.9   170 2   A60037   vasoactive
intesti
     11   62   55.9   195 2   I50456   pituitary
adenylat
     12   61   55.0   176 2   I84638   pituitary
adenylat
     13   60   54.1   44 1   RHBOS   somatoliberin

Title: US-10-009-643-5
Perfect score: 111
Sequence: 1 SKAYRKLLGQLSARLYLHSLMAK 23

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 500 summaries

Database :   UniProt_03:*
                 1: uniprot_sprot:*
                 2: uniprot_trembl:*

                              SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	104	93.7	175	1	PACA_CHICK	P41534 g glucagon-
2	97	87.4	173	1	PACA_ONCNE	P41585 oncorhynchu
3	97	87.4	173	2	Q98SP5	Q98sp5 oncorhynchu
4	94	84.7	45	1	SLIB_CYPCA	P42692 cyprinus ca
5	94	84.7	89	2	Q98SP6	Q98sp6 anas platyr
6	94	84.7	171	1	PACA_RANRI	Q09169 r glucagon-
7	94	84.7	172	2	Q9DE29	Q9de29 brachydanio
8	81	73.0	176	1	PACA_PIG	P41535 s pituitary
9	80	72.1	176	1	PACA_SHEEP	P16613 o pituitary
10	78	70.3	171	2	Q9PUF8	Q9puf8 xenopus lae
11	71	64.0	175	1	PACA_RAT	P13589 r pituitary

```
Run on:          March 26, 2005, 01:33:19 ; Search time 314 Seconds
                                           (without alignments)
                                           8801.501 Million cell
updates/sec

Title:           US-10-009-643-3
Perfect score:   1689
Sequence:        1 taaggaagataaaagaatta..........atactcagtcttcacacaga
1689

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters:        2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       Issued_Patents_NA:*
                 1:  /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
                 2:  /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
                 3:  /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
                 4:  /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
                 5:  /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                 6:  /cgn2_6/ptodata/1/ina/backfiles1.seq:*

                            SUMMARIES
                     %
Result           Query
   No.    Score   Match  Length  DB   ID                      Description

-------------------------------------------------------------------------
----
     1    484.6   28.7   1272   1   US-08-073-799C-7          Sequence 7,
Appli
     2    484.6   28.7   1272   1   US-07-947-672-7           Sequence 7,
Appli
     3    484.6   28.7   1272   1   US-08-432-043-7           Sequence 7,
Appli
     4    484.6   28.7   1272   2   US-08-660-963-7           Sequence 7,
Appli
     5    481.8   28.5   1617   4   US-09-016-434-1211        Sequence
1211, Ap
     6    474.8   28.1   1257   1   US-07-946-232-7           Sequence 7,
Appli
     7    469.6   27.8   1545   2   US-08-660-963-9           Sequence 9,
Appli
     8    446.2   26.4   1983   1   US-08-073-799C-9          Sequence 9,
Appli
     9    296.4   17.5   1455   2   US-08-811-897A-31         Sequence 31,
Appl
    10    296.4   17.5   1455   2   US-08-855-213-31          Sequence 31,
```

```
Run on:            March 26, 2005, 01:53:48 ; Search time 926 Seconds
                                            (without alignments)
                                            10869.667 Million cell
updates/sec

Title:             US-10-009-643-3
Perfect score:     1689
Sequence:          1 taaggaagataaaagaatta..........atactcagtcttcacacaga
1689

Scoring table:     IDENTITY_NUC
                   Gapop 10.0 , Gapext 1.0

Searched:          5552208 seqs, 2979665951 residues

Total number of hits satisfying chosen parameters:        11104416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :         Published_Applications_NA:*
                   1:  /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
                   2:  /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
                   3:  /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
                   4:  /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
                   5:  /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
                   6:  /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
                   7:  /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
                   8:  /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
                   9:  /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
                   10:  /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
                   11:  /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
                   12:  /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
                   13:  /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
                   14:  /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
                   15:  /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
                   16:  /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
                   17:  /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
                   18:  /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
                   19:  /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
                   20:  /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
                   21:  /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
                   22:  /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*
```

                               SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	481.8	28.5	1617	14	US-10-147-087-3	Sequence 3, Appli
2	481.8	28.5	1617	15	US-10-171-581-230	Sequence 230, App
3	481.8	28.5	1617	15	US-10-225-567A-141	Sequence

```
Run on:            March 26, 2005, 01:26:25 ; Search time 5069 Seconds
                                            (without alignments)
                                            12683.084 Million cell
updates/sec

Title:             US-10-009-643-3
Perfect score:     1689
Sequence:          1 taaggaagataaaagaatta..........atactcagtcttcacacaga
1689

Scoring table:     IDENTITY_NUC
                   Gapop 10.0 , Gapext 1.0

Searched:          34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters:       68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :         EST:*
                   1:  gb_est1:*
                   2:  gb_est2:*
                   3:  gb_htc:*
                   4:  gb_est3:*
                   5:  gb_est4:*
                   6:  gb_est5:*
                   7:  gb_est6:*
                   8:  gb_gss1:*
                   9:  gb_gss2:*

                                SUMMARIES
                   %
Result             Query
   No.    Score  Match Length DB   ID                    Description

------------------------------------------------------------------------
----
       1     485   28.7    621  4  BM490642              BM490642
pgp2n.pk0
       2   437.4   25.9   1551  3  AK030504              AK030504 Mus
muscu
       3   412.2   24.4   1272  9  AY416892              AY416892 Homo
sapi
       4   394.6   23.4   1272  9  AY416894              AY416894 Mus
muscu
       5     355   21.0   1146  9  AY416893              AY416893 Pan
trogl
       6   292.6   17.3   1407  9  AY400569              AY400569 Homo
sapi
       7   291.4   17.3   1407  9  AY400570              AY400570 Pan
trogl
       8     291   17.2   2583  3  AK052465              AK052465 Mus
muscu
       9   286.8   17.0   1407  9  AY400571              AY400571 Mus
muscu
```

Run on: March 26, 2005, 14:27:54 ; Search time 71 Seconds
                                            (without alignments)
                                            2282.431 Million cell
updates/sec

Title: US-10-009-643-4
Perfect score: 2272
Sequence: 1 MSYHCVLYTLTLAVLVAGNV.........RRTRWTVPTSSGVKMNTSVC 419

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   A_Geneseq_16Dec04:*
                 1: geneseqp1980s:*
                 2: geneseqp1990s:*
                 3: geneseqp2000s:*
                 4: geneseqp2001s:*
                 5: geneseqp2002s:*
                 6: geneseqp2003as:*
                 7: geneseqp2003bs:*
                 8: geneseqp2004s:*

                            SUMMARIES
                 %
Result   Query
   No.   Score   Match Length DB ID   Description

----
      1   2272 100.0   419 4 AAB19981   Aab19981
Chicken g
      2 1419.5   62.5   423 2 AAR51072   Aar51072
Human Gro
      3 1419.5   62.5   423 2 AAW10488   Aaw10488
Human acr
      4 1419.5   62.5   423 2 AAW24033   Aaw24033
Growth ho
      5 1419.5   62.5   423 2 AAW67744   Aaw67744
Human clo
      6 1419.5   62.5   423 4 AAB71873   Aab71873
Human GRF
      7 1419.5   62.5   423 7 ADC86187   Adc86187
Human GPC
      8 1419.5   62.5   423 8 ADH34649   Adh34649
Growth ho
      9 1419.5   62.5   423 8 ADO29355   Ado29355

Run on: March 26, 2005, 14:31:19 ; Search time 21 Seconds
                                        (without alignments)
                                        1489.427 Million cell
updates/sec

Title: US-10-009-643-4
Perfect score: 2272
Sequence: 1 MSYHCVLYTLTLAVLVAGNV.........RRTRWTVPTSSGVKMNTSVC 419

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents_AA:*
                 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
                 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
                 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
                 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
                 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

                           SUMMARIES

              %
Result   Query
  No.   Score Match Length DB ID   Description

----
     1 1419.5 62.5   423 1 US-08-073-799C-8   Sequence 8,
Appli
     2 1419.5 62.5   423 1 US-07-947-672-8   Sequence 8,
Appli
     3 1419.5 62.5   423 1 US-08-432-043-8   Sequence 8,
Appli
     4 1419.5 62.5   423 2 US-08-660-963-8   Sequence 8,
Appli
     5 1419.5 62.5   423 4 US-09-631-603-18   Sequence 18,
Appl
     6 1397.5 61.5   418 1 US-07-946-232-8   Sequence 8,
Appli
     7 1313.5 57.8   513 2 US-08-660-963-11   Sequence 11,
Appl
     8   1313 57.8   457 2 US-08-660-963-10   Sequence 10,
Appl
     9   1035 45.6   459 4 US-09-694-519-4   Sequence 4,
Appli
    10   1012 44.5   459 4 US-09-694-519-3   Sequence 3,
Appli
    11   1012 44.5   459 4 US-09-694-519-8   Sequence 8,
Appli

```
Run on:            March 26, 2005, 14:32:59 ; Search time 50 Seconds
                                            (without alignments)
                                            2774.626 Million cell
updates/sec

Title:             US-10-009-643-4
Perfect score:     2272
Sequence:          1 MSYHCVLYTLTLAVLVAGNV.........RRTRWTVPTSSGVKMNTSVC 419

Scoring table:     BLOSUM62
                   Gapop 10.0 , Gapext 0.5

Searched:          1407402 seqs, 331100923 residues

Total number of hits satisfying chosen parameters:        1407402

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :         Published_Applications_AA:*
                   1:   /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
                   2:   /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
                   3:   /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
                   4:   /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
                   5:   /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
                   6:   /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
                   7:   /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
                   8:   /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
                   9:   /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
                   10:  /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
                   11:  /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
                   12:  /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
                   13:  /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
                   14:  /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
                   15:  /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
                   16:  /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
                   17:  /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
                   18:  /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
                   19:  /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
                   20:  /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

                             SUMMARIES
                    %
Result             Query
   No.    Score   Match  Length DB  ID                      Description

------------------------------------------------------------------------
----
     1  1419.5    62.5    423   15  US-10-292-798-640           Sequence
 640, App
     2  1414.5    62.3    423   14  US-10-147-087-4          Sequence 4,
Appli
     3  1414.5    62.3    423   14  US-10-225-567A-142          Sequence
 142, App
     4  1243      54.7    476   14  US-10-017-161-730           Sequence
 730, App
```

```
Run on:           March 26, 2005, 14:30:29 ; Search time 16 Seconds
                                            (without alignments)
                                            2519.676 Million cell
updates/sec

Title:            US-10-009-643-4
Perfect score:    2272
Sequence:         1 MSYHCVLYTLTLAVLVAGNV..........RRTRWTVPTSSGVKMNTSVC 419

Scoring table:    BLOSUM62
                  Gapop 10.0 , Gapext 0.5

Searched:         283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters:      283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :        PIR_79:*
                  1:  pir1:*
                  2:  pir2:*
                  3:  pir3:*
                  4:  pir4:*
                                          SUMMARIES
                  %
Result            Query
  No.     Score  Match Length DB  ID                    Description

--------------------------------------------------------------------------
----
      1  1414.5   62.3    423  2  A45363                somatoliberin
rece
      2  1352.5   59.5    451  2  I46586                growth
hormone-rel
      3  1274.5   56.1    464  2  S29754                growth
hormone-rel
      4   1274    56.1    423  2  S29753                growth
hormone-rel
      5   1012    44.5    459  2  JH0594                vasoactive
intesti
      6   985.5   43.4    467  2  JN0616                pituitary
adenylat
      7   977.5   43.0    525  2  JN0902                pituitary
adenylat
      8    973    42.8    495  2  JC2195                vasoactive
intesti
      9   971.5   42.8    460  2  JC2194                vasoactive
intesti
     10   961.5   42.3    495  2  S39061                pituitary
```

Run on: March 26, 2005, 14:29:49 ; Search time 58 Seconds
                                           (without alignments)
                                           3699.331 Million cell
updates/sec

Title: US-10-009-643-4
Perfect score: 2272
Sequence: 1 MSYHCVLYTLTLAVLVAGNV..........RRTRWTVPTSSGVKMNTSVC 419

Scoring table: BLOSUM62
                  Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   UniProt_03:*
                  1: uniprot_sprot:*
                  2: uniprot_trembl:*

                                    SUMMARIES
                     %
Result   Query
  No.   Score   Match Length DB   ID   Description

----
     1 1419.5   62.5   423   1   GRFR_HUMAN   Q02643 homo
sapien
     2 1366.5   60.1   423   1   GRFR_PIG   P34999 sus
scrofa
     3   1365   60.1   423   2   Q9BDH9   Q9bdh9 bos
taurus
     4   1360   59.9   423   2   Q9N1F8   Q9n1f8 bos
taurus
     5   1339   58.9   441   2   Q9TUJ0   Q9tuj0 bos
taurus
     6   1313   57.8   407   2   Q9BDI0   Q9bdi0 ovis
aries
     7   1297   57.1   439   2   Q9WU99   Q9wu99 rattus
norv
     8 1279.5   56.3   464   1   GRFR_RAT   Q02644 rattus
norv
     9 1274.5   56.1   464   2   Q6LEF5   Q6lef5 rattus
sp.
    10   1274   56.1   423   1   GRFR_MOUSE   P32082 mus